

Python - Control structures

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Availability of slides

- All materials are freely available (CC BY) after the lectures:
 - StudIP: 'Python for Life Scientists'
 - GitHub: https://github.com/bpucker/teaching
- Questions: Feel free to ask at any time
- Feedback, comments, or questions: b.pucker[a]tu-bs.de

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If & else

- Distinguish between two cases
- Action depends on result of comparison

```
a = 5 #define variable
#user inputs number
b = int( input("please enter number!") )
if b < a:#if b is smaller than a
    print("b is smaller than a")
else:
    print("b is NOT smaller than a")</pre>
```

please enter number!3
b is smaller than a



elif

- Distinguish between multiple cases
- Action depends on result of comparison

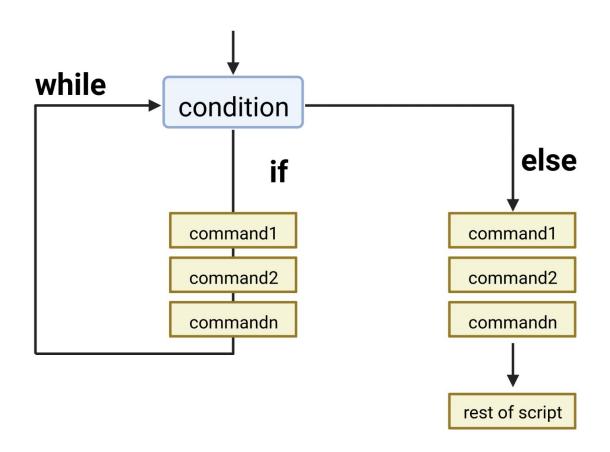
```
a = 5 #define variable
#user inputs number
b = int( input("please enter number!") )
if b < a:#if b is smaller than a
    print("b is smaller than a")
elif b == a:
    print("b is matching a")
else:
    print("b is bigger than a")</pre>
```

Exercises - Part3a

- 3.1) Write a script for guessing numbers!
- 3.2) Add tips (smaller/larger) during the guessing process!



Concept of loops





While loop (example)

```
a = 0
    while a < 10: #checks if a is smaller than 10</pre>
         print(str( a ) + " is smaller than 10")
          a += 1 \# a = a+1
 5
         #something useful could happen here
print("a was increased by 1")
 67
    print(str( a ) + "is larger than 10")
  Code is executed until the
condition for this loop becomes
            false
```

While infinite loop

WARNING: this loop is infinite!

```
#infinite loop:
a = 0

while True: #always true
a += 1 #a = a+1
print(str(a))
print("this line is never reached")
```

For loop

```
Control variable (species)

List of data (list_of_species)

list_of_species = [ "E.coll", "B.subtilis", "S.cerevisiae", "C.glutamicum", "A.tumefaciens"

for species in list_of_species:
    if len( species ) < 12: #Length of names is calculated and compared
        print(species) #Name is printed

#Line 3+4 is executed several times:

#1: species = "E.coli"

#2: species = "B.subtilis"

#3: species = "S.cerevisiae"

Species name is printed if shorter than 12 characters
```

Exercises - Part3b

- 3.3) Write a function counting to 100 and printing all number which can be divided by 4 without any residue!
 - Info: 10%2 #modulo division in Python
- 3.4) Write a function counting down from 1000 to 0 and printing all numbers!
- 3.5) Generate a list of species names! Write a function that prints all species names starting with 'E'!
- 3.6) Expand this function to limit the printing to species names which are additionally shorter than 10 characters!
- 3.7) Expand this function to limit the printing to species names which are additionally ending with 'a'.

Exercises - Part3b (addition)

- X1: Print species names that match at least 2 of the following 3 conditions: (1) longer than 8 characters, (2) start with 'E', (3) end with 'a'
- X2: Print species names that are identical to the previous or next species name in the list.



range()

```
list of species = ["E.coli", "B.subtilis", "S.cerevisiae", "C.glutamicum", "A.tumefaciens"]
   length = len( list of species ) #length = 5
   pfor i in range( length ): #starts at 0 and runs to i=4 (five values)
 4
        if len( list of species[ i ] ) < 12: #length of name is calculated and compared</pre>
 5
            print(list of species[ i ]) #name is printed
 6
 7
   #i is taking five different values:
 8
   #1: i=0
   #2: i=1
   #3: i=2
11
   #4: i=3
12
  #5: i=4
13 #i=5 is never reached by range()
```

enumerate()

Exercises - Part3c

- 3.8) Write a script to print 50x 'here' and the current value of the control variable!
- 3.9) Write a script to walk through the species list and to print the character from the species where the index corresponds to the current control variable value!

Checking a list/string for a sublist/substring

Check if an element is contained in a list:

```
genes = ["g1", "g2", "g3", "g4", "g5"]
if "g3" in genes:
    print("g3 in genes")

g3 in genes
```

Check if a substring is contained in a string:

```
genome_seq = "ACACCGATTACTGGAGGTTACGTAATGGCCA"
primer = "ACTGGAGGTTACG"
if primer in genome_seq:
    print("primer binding site detected.")
else:
    print("no primer binding site detected")
```

primer binding site detected.



Time for questions!

